

## SEQLIST\_DAVI257.002APC.TXT

## SEQUENCE LISTING

<110> Hart, Derek Nigel John  
Kato, Masato

<120> DEC-205 (LY 75)/DCL-1 INTERGENIC SPLICE VARIANTS ASSOCIATED WITH HODGKIN'S DISEASE, AND USES THEREOF

<130> DAVI257.002APC

<140> US 10/537,839  
<141> 2005-06-06

<150> PCT/AU03/01634  
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<151> 2002-12-06

<160> 32

<170> PatentIn version 3.1

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<212> DNA  
<213> mammalian

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Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
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Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn			
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1085 1090 1095			

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Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Thr Lys Cys Gln	
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Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys	
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Phe	Gly	Arg	Val	Val	Cys	Lys	Val	Pro	Leu	Asp	Cys	Pro	Ser	Ser	
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gat	atc	cta	cta	ggc	atg	ttt	tat	gac	aca	gat	gat	gcg	agt	ttc	5229
Asp	Ile	Leu	Leu	Gly	Met	Phe	Tyr	Asp	Thr	Asp	Asp	Ala	Ser	Phe	
1730						1735					1740				
aag	tgg	ttt	gat	aat	tca	aat	atg	aca	ttt	gat	aag	tgg	aca	gac	5274
Lys	Trp	Phe	Asp	Asn	Ser	Asn	Met	Thr	Phe	Asp	Lys	Trp	Thr	Asp	
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caa	gat	gat	gat	gag	gat	tta	gtt	gac	acc	tgt	gct	ttt	ctg	cac	5319
Gln	Asp	Asp	Asp	Glu	Asp	Leu	Val	Asp	Thr	Cys	Ala	Phe	Leu	His	
1760						1765					1770				
atc	aag	aca	ggt	gaa	tgg	aaa	aaa	gga	aat	tgt	gaa	gtt	tct	tct	5364
Ile	Lys	Thr	Gly	Glu	Trp	Lys	Lys	Gly	Asn	Cys	Glu	Val	Ser	Ser	
1775						1780					1785				
gtg	gaa	gga	aca	cta	tgc	aaa	aca	gct	atc	cca	tac	aaa	agg	aaa	5409
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tac aaa aaa cat tct gat tct cgt ttc acc aca gtt ttt tca acc Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr Val Phe Ser Thr 1835 1840 1845			5544
gca ccc caa tca cct tat aat gaa gac tgt gtt ttg gta gtt gga Ala Pro Gln Ser Pro Tyr Asn Glu Asp Cys Val Leu Val Val Gly 1850 1855 1860			5589
gaa gaa aat gaa tat cct gtt caa ttt gac taa Glu Glu Asn Glu Tyr Pro Val Gln Phe Asp 1865 1870			5622
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<p>Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp 50 55 60</p>			
<p>Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser 65 70 75 80</p>			
<p>Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg 85 90 95</p>			
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<p>His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly 115 120 125</p>			

SEQLIST\_DAVI257.002APC.TXT

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly  
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Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp  
165 170 175

Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro  
180 185 190

Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile  
195 200 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu  
210 215 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp  
225 230 235 240

Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser  
245 250 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile  
260 265 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly  
275 280 285

Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro  
290 295 300

Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met  
305 310 315 320

Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu  
325 330 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp  
340 345 350

\* Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn  
355 360 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys  
370 375 380

SEQLIST\_DAVI257.002APC.TXT

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His  
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Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp  
405 410 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr  
420 425 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp  
435 440 445

Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser  
450 455 460

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys  
465 470 475 480

Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser  
485 490 495

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu  
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Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys  
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Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu  
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Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu  
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Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly  
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Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala  
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Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys  
595 600 605

Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys  
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Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp  
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Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys  
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Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu  
660 665 670

Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe  
675 680 685

Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln  
690 695 700

Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro  
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Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr  
725 730 735

Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys  
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Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe  
755 760 765

Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr  
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Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr  
785 790 795 800

Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu  
805 810 815

Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn  
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Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala  
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Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala  
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SEQLIST\_DAVI257.002APC.TXT

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Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe  
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Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp  
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Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe  
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Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp  
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Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn  
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Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala  
965 970 975

Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser  
980 985 990

Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala  
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Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn  
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Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro  
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Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu  
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Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys  
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Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg  
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His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg  
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Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn  
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SEQLIST\_DAVI257.002APC.TXT

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Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp  
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Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn  
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Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn  
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Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala  
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Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp  
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Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala  
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Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro  
1220 1225 1230

Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp  
1235 1240 1245

Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn  
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Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln  
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Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys  
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Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met  
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Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu  
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Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala  
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## SEQLIST\_DAVI257.002APC.TXT

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Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu  
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Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe  
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Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val  
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Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His  
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Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp  
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Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu Ser Ser  
 1445 1450 1455

His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly Ser Thr  
 1460 1465 1470

Phe Asp Tyr Ile Pro Trp Lys Gly Gln Thr Ser Pro Gly Asn Cys  
 1475 1480 1485

Val Leu Leu Asp Pro Lys Gly Thr Trp Lys His Glu Lys Cys Asn  
 1490 1495 1500

Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Ser Lys  
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Lys Leu Ser Arg Leu Thr Tyr Ser Ser Arg Cys Pro Ala Ala Lys  
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Glu Asn Gly Ser Arg Trp Ile Gln Tyr Lys Gly His Cys Tyr Lys  
 1535 1540 1545

Ser Asp Gln Ala Leu His Ser Phe Ser Glu Ala Lys Lys Leu Cys  
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Ser Lys His Asp His Ser Ala Thr Ile Val Ser Ile Lys Asp Glu  
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SEQLIST\_DAVI257.002APC.TXT

Asp Glu Asn Lys Phe Val Ser Arg Leu Met Arg Glu Asn Asn Asn  
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Ile Thr Met Arg Val Trp Leu Gly Leu Ser Gln His Ser Val Asp  
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Gln Ser Trp Ser Trp Leu Asp Gly Ser Glu Val Thr Phe Val Lys  
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Trp Glu Asn Lys Ser Lys Ser Gly Val Gly Arg Cys Ser Met Leu  
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Ile Ala Ser Asn Glu Thr Trp Lys Lys Val Glu Cys Glu His Gly  
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Phe Gly Arg Val Val Cys Lys Val Pro Leu Asp Cys Pro Ser Ser  
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Thr Trp Ile Gln Phe Gln Asp Ser Cys Tyr Ile Phe Leu Gln Glu  
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Ala Ile Lys Val Glu Ser Ile Glu Asp Val Arg Asn Gln Cys Thr  
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Asp His Gly Ala Asp Met Ile Ser Ile His Asn Glu Glu Glu Asn  
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Ala Phe Ile Leu Asp Thr Leu Lys Lys Gln Trp Lys Gly Pro Asp  
1715 1720 1725

Asp Ile Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe  
1730 1735 1740

Lys Trp Phe Asp Asn Ser Asn Met Thr Phe Asp Lys Trp Thr Asp  
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Gln Asp Asp Asp Glu Asp Leu Val Asp Thr Cys Ala Phe Leu His  
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Ile Lys Thr Gly Glu Trp Lys Lys Gly Asn Cys Glu Val Ser Ser  
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Val Glu Gly Thr Leu Cys Lys Thr Ala Ile Pro Tyr Lys Arg Lys  
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## SEQLIST\_DAVI257.002APC.TXT

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Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile Ile Trp Phe Leu  
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Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr Val Phe Ser Thr  
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Lys Gln Trp Lys Gly Pro Asp Asp Ile Leu Leu Gly Met Phe Tyr Asp  
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ctggatcaac tatggacacc aaaagacatg tggttctgtc cacttacccctt tttccctta	780
acactttaga gaagacacctt cccttgtgaa acgtttcgctt gttagggtat actgttcttc	840
ataaaatagtc tattgggtgtt aaattatagc tgagaccactt agcgatcgtt tcattgagac	900
cgtcaaaacc ctcgctagta aaccaaggag atatcttctt tgccgcgcgag accgaagtgg	960
agaaaaaagt gacgtgggtga cagtgaaatg tcactaccga cacgggacca tcaacgtctt	1020
cttctactta tacgacaagt cgacctgatt ctcaaaccat tatagtccgg tcgtataact	1080
yaggttaactg ttwttaaagg acacgttcca aaagtatatt tt	1122

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<212> DNA  
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<220>  
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<222> (1)..(672)

<220>  
<221> VARIANT  
<222> (5)..(5)  
<223> Xaa = Leu

<220>  
<221> VARIANT  
<222> (13)..(13)  
<223> Xaa = Val, Ala

<220>  
<221> VARIANT  
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<223> Xaa = Thr

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His Glu Ala Ser Xaa Val Leu Leu Ser Leu Ala Thr Xaa Ile Phe Ala			
1	5	10	15
gac tgt cct tcg tcc atc tgg gtt cag ttc caa ggc agc tgt tac act			96
Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr			
20	25	30	
ttt ctt caa gta acc atc aat gtg gaa aac ata gag gat gtc aga aag			144
Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys			
35	40	45	
cag tgt act gat cac ggg gca gac ctg gta agt ata cac aat gaa gaa			192
Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu			
50	55	60	
gaa aac gca ttt ata ctg gac act tta caa aag cga tgg aaa ggc ccg			240
Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro			
65	70	75	80
gat gat ctt ctg cta ggc atg ttt tat gac act gat gat gca agt ttc			288
Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe			
85	90	95	
aag tgg ttt gat cag tca aat atg aca ttc gac aag tgg gca gat gag			336
Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu			
100	105	110	
gat ggt gag gac cta gtt gac acc ttt ggt ttt ctg tat gcc aag aca			384
Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr			
115	120	125	
ggt gaa tgg aga aaa gga aat tgt gaa atg tct tct gtg acr gga aca			432
Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr			
130	135	140	
ctt tgc aaa aca gca atc cca tat gac aag aag tat tta tca gat aac			480
Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn			
145	150	155	160
cac att tta ata tcg act ctg gtg atc gct agc aca gtg act ctg gca			528
His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala			
165	170	175	
gtt ttg gga gcg gtc att tgg ttc ctc tat aga agg agc gca cgc tct			576
Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser			
180	185	190	
ggc ttc acc tct ttc tct cct gca cca caa tca cct tac agt gat ggc			624
Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly			
195	200	205	
tgt gct ctg gta gtt gcg gaa gaa gat gaa tac tct gtt cag ctg gac			672
Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp			
210	215	220	
tgagagttt ggaacatcatcg acgagcacac tgaacaccc ttgaaat aatttccttat			732
gcaagattgt catgtaaaat ttgccacgga aaactgaacc ttttatggta ttccttattc			792
ttcttaacaat attttcatgtt attcaatgtg acaaaaacata aaccttctga ttaaaaggaa			852

SEQLIST\_DAVI257.002APC.TXT

aaaaagtagg tttcagaaaa ggaactagca cagagctaac ttacaggttt tcttaagtag	912
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aaaaaaaa	979
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<223> Xaa = Leu	
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<223> Xaa = Ala or Val	
<220>	
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<222> (142)..(142)	
<223> Xaa = Thr	
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His Glu Ala Ser Xaa Val Leu Leu Ser Leu Ala Thr Xaa Ile Phe Ala	
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Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr	
20 25 30	
Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys	
35 40 45	
Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu	
50 55 60	
Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro	
65 70 75 80	
Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe	
85 90 95	
Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu	
100 105 110	
Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr	
115 120 125	
Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr	
130 135 140	

SEQLIST\_DAVI257.002APC.TXT

Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn  
145 150 155 160

His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala  
165 170 175

Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser  
180 185 190

Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly  
195 200 205

Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp  
210 215 220

<210> 12

<211> 979

<212> DNA

<213> mammalian

<400> 12

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cttttgtatc tcctacagtc tttcgtcaca tgactagtgc cccgtctgga ccattcatat 180  
gtgttacttc ttctttgcg taaatatgac ctgtgaaatg tttcgctac cttccggc 240  
ctactagaag acgatccgta caaaaatactg tgactactac gttcaaagtt caccaaacta 300  
gtcagtttat actgtaaagct gttcacccgt ctactcctac cactcctgga tcaactgtgg 360  
acacccaaag acatacggtt ctgtccactt acctctttc cttAACACT ttacagaaga 420  
cactgycctt gtgaaacggtt ttgtcgtag ggtatactgt tcttcataaa tagtctattg 480  
gtgtaaaatt atagctgaga ccactagcga tcgtgtcact gagaccgtca aaaccctcgc 540  
cagtaaacca aggagatatc ttcctcgcgt gcgagaccga agtggagaaa gagaggacgt 600  
ggtgttagtg gaatgtcact accgacacga gaccatcaac gccttcttct acttatgaga 660  
caagtcgacc tgactctcaa accctttag tctgctcgtag tgacttgg aactgttctt 720  
tattaaagga tacgttctaa cagtagattaa taaacggtagtgc ctttgactt ggaaaatacc 780  
ataaggaata agaagattgt tataaaagta cataagttac actgtttgtt atttgaaaga 840  
ctaattttcc ttttttcat ccaaagtctt ttccttgatc gtgtctcgat tgaatgtcca 900  
aaagaattca tcaaaagtaa actcatttac tttcgatgtc atgttatttc gaccatttg 960  
cgttttttt tttttttt 979

SEQLIST\_DAVI257.002APC.TXT

<210> 13  
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<212> DNA  
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<220>  
<221> misc\_feature  
<222> (43)..(43)  
<223> n = A, C, G or T

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atatttatca gataaccgca ttttaatatc agctttggtg attgcttagca cagtaattct 180  
gacagttctg ggagcagttg tttggttctt gtacaaaaga agtttggatt ctggtttcac 240  
cacagtttt tcagctgcac accaatcacc ttataatgat gactgtgttt tagtagttgc 300  
agaggaaaac gaatatgata ttcaatttaa ctaagatttt ggaaatatca gactaagaca 360  
aatacccttc agtgattcct ctgtaagatt tcaatataaa acctgataat gaaaattagt 420  
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Lys Val Pro Leu Gly Pro Asp Tyr Thr  
1 5

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<213> mammalian

<400> 15

Lys Val Pro Leu Gly Pro Asp Tyr Thr  
1 5

<210> 16  
<211> 42  
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<213> mammalian

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<221> CDS

<222> (1)...(42)

<400> 16

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42

<210> 17

<211> 14

<212> PRT

<213> mammalian

<400> 17

Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe  
1 5 10

<210> 18

<211> 42

<212> DNA

<213> mammalian

<220>

<221> CDS

<222> (1)...(42)

<400> 18

gct gcc gtc gcg gac tgt cct tca tct act tgg att cag ttc  
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1 5 10

42

<210> 19

<211> 14

<212> PRT

<213> mammalian

<400> 19

Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe  
1 5 10

<210> 20

<211> 5454

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<220>

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<222> (1)...(5451)

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1 5 10 15			
ctg ctc ttc tgg ttc gat ctc gcg gag ccc tct ggc cgc gca gct			96
Leu Leu Phe Trp Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala			
20 25 30			
aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag			144
Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys			
35 40 45			
cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac			192
Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp			
50 55 60			
aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc			240
Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser			
65 70 75 80			
caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga			288
Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg			
85 90 95			
atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac			336
Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His			
100 105 110			
cac tct ctg tac gga gct gcc cggt tac cgg ctg gct ctg aag gat gga			384
His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly			
115 120 125			
cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc			432
His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly			
130 135 140			
tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga			480
Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg			
145 150 155 160			
gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat			528
Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp			
165 170 175			
ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca			576
Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro			
180 185 190			
tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc			624
Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile			
195 200 205			
tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag			672
Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu			
210 215 220			
cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg			720
Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp			
225 230 235 240			

## SEQLIST\_DAVI257.002APC.TXT

aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser 245 250 255	768
atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile 260 265 270	816
gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly 275 280 285	864
tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro 290 295 300	912
gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met 305 310 315 320	960
gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu 325 330 335	1008
ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp 340 345 350	1056
gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn 355 360 365	1104
aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys 370 375 380	1152
gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His 385 390 395 400	1200
tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat Ser Leu Ala Asp Val Glu Val Val Thr Lys Leu His Asn Glu Asp 405 410 415	1248
atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr 420 425 430	1296
tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp 435 440 445	1344
gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser 450 455 460	1392
tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys 465 470 475 480	1440
cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser 485 490 495	1488

SEQLIST\_DAVI257.002APC.TXT

tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg Arg His Gly Glu 500 505 510	1536
acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys 515 520 525	1584
aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu 530 535 540	1632
atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu 545 550 555 560	1680
aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly 565 570 575	1728
aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala 580 585 590	1776
tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys 595 600 605	1824
tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys 610 615 620	1872
aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp 625 630 635 640	1920
gac ccc tgt cct gaa ggc tgg cag agt ttc ccc gca agt ctt tct tgt Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys 645 650 655	1968
tat aag gta ttc cat gca gaa aga att gta aga aag agg aac tgg gaa Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu 660 665 670	2016
gaa gct gaa cga ttc tgc caa gcc ctt gga gca cac ctt tct agc ttc Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe 675 680 685	2064
agc cat gtg gat gaa ata aag gaa ttt ctt cac ttt tta acg gac cag Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln 690 695 700	2112
ttc agt ggc cag cat tgg ctg tgg att ggt ttg aat aaa agg agc cca Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro 705 710 715 720	2160
gat tta caa gga tcc tgg caa tgg agt gat cgt aca cca gtg tct act Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr 725 730 735	2208

## SEQLIST\_DAVI257.002APC.TXT

att atc atg cca aat gag ttt cag cag gat tat gac atc aga gac tgt Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys 740 745 750	2256
gct gct gtc aag gta ttt cat agg cca tgg cga aga ggc tgg cat ttc Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe 755 760 765	2304
tat gat gat aga gaa ttt att tat ttg agg cct ttt gct tgt gat aca Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr 770 775 780	2352
aaa ctt gaa tgg gtg tgc caa att cca aaa ggc cgt act cca aaa aca Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr 785 790 795 800	2400
cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu 805 810 815	2448
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn 820 825 830	2496
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala 835 840 845	2544
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala 850 855 860	2592
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp 865 870 875 880	2640
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe 885 890 895	2688
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp 900 905 910	2736
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe 915 920 925	2784
atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp 930 935 940	2832
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn 945 950 955 960	2880
aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala 965 970 975	2928
agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser 980 985 990	2976

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cag att gaa caa gac ttt att aca	tcc ttg ctt ccg gat	atg gaa gct	3024
Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp	Leu Pro Asp	Met Glu Ala	
995	1000	1005	
act tta tgg att ggt ttg cgc	tgg act gcc tat gaa	aag ata aac	3069
Thr Leu Trp Ile Gly Leu Arg	Trp Thr Ala Tyr Glu	Lys Ile Asn	
1010	1015	1020	
aaa tgg aca gat aac aga gag	ctg acg tac agt aac	ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu	Leu Thr Tyr Ser Asn	Phe His Pro	
1025	1030	1035	
tta ttg gtt agt ggg agg ctg	aga ata cca gaa aat	ttt ttt gag	3159
Leu Leu Val Ser Gly Arg Leu	Arg Ile Pro Glu Asn	Phe Phe Glu	
1040	1045	1050	
gaa gag tct cgc tac cac tgg	gcc cta ata ctc aac	ctc caa aaa	3204
Glu Glu Ser Arg Tyr His Cys	Ala Leu Ile Leu Asn	Leu Gln Lys	
1055	1060	1065	
tca ccg ttt act ggg acg tgg	aat ttt aca tcc tgc	agt gaa cgc	3249
Ser Pro Phe Thr Gly Thr Trp	Asn Phe Thr Ser Cys	Ser Glu Arg	
1070	1075	1080	
cac ttt gtg tct ctc tgt cag	aaa tat tca gaa gtt	aaa agc aga	3294
His Phe Val Ser Leu Cys Gln	Lys Tyr Ser Glu Val	Lys Ser Arg	
1085	1090	1095	
cag acg ttg cag aat gct tca	gaa act gta aag tat	cta aat aat	3339
Gln Thr Leu Gln Asn Ala Ser	Glu Thr Val Lys Tyr	Leu Asn Asn	
1100	1105	1110	
ctg tac aaa ata atc cca aag	act ctg act tgg cac	agt gct aaa	3384
Leu Tyr Lys Ile Ile Pro Lys	Thr Leu Thr Trp His	Ser Ala Lys	
1115	1120	1125	
agg gag tgt ctg aaa agt aac	atg cag ctg gtg agc	atc acg gac	3429
Arg Glu Cys Leu Lys Ser Asn	Met Gln Leu Val Ser	Ile Thr Asp	
1130	1135	1140	
cct tac cag cag gca ttc ctc	agt gtg cag gcg ctc	ctt cac aac	3474
Pro Tyr Gln Gln Ala Phe Leu	Ser Val Gln Ala Leu	Leu His Asn	
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tct tcc tta tgg atc gga ctc	ttc agt caa gat gat	gaa ctc aac	3519
Ser Ser Leu Trp Ile Gly Leu	Phe Ser Gln Asp Asp	Glu Leu Asn	
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Phe Gly Trp Ser Asp Gly Lys	Arg Leu His Phe Ser	Arg Trp Ala	
1175	1180	1185	
gaa act aat ggg caa ctc gaa	gac tgt gta gta tta	gac act gat	3609
Glu Thr Asn Gly Gln Leu Glu	Asp Cys Val Val Leu	Asp Thr Asp	
1190	1195	1200	
gga ttc tgg aaa aca gtt gat	tgc aat gac aat caa	cca ggt gct	3654
Gly Phe Trp Lys Thr Val Asp	Cys Asn Asp Asn Gln	Pro Gly Ala	
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Val	Asp	Ser	Val	Lys	Cys	Pro	Ser	Pro	Val	Leu	Asn	Thr	Pro	Trp		
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Ile	Pro	Phe	Gln	Asn	Cys	Cys	Tyr	Asn	Phe	Ile	Ile	Thr	Lys	Asn		
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Glu	Asn	Asn	Phe	Val	Leu	Glu	Gln	Leu	Leu	Tyr	Phe	Asn	Tyr	Met		
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Ala	Ser	Trp	Val	Met	Leu	Gly	Ile	Thr	Tyr	Arg	Asn	Asn	Ser	Leu		
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Met	Trp	Phe	Asp	Lys	Thr	Pro	Leu	Ser	Tyr	Thr	His	Trp	Arg	Ala		
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Thr	Asp	Gly	Phe	Trp	Asp	Ile	Gln	Thr	Phe	Lys	Val	Ile	Glu	Glu		
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Phe	Asp	Tyr	Ile	Pro	Trp	Lys	Gly	Gln	Thr	Ser	Pro	Gly	Asn	Cys				
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Val	Leu	Leu	Asp	Pro	Lys	Gly	Thr	Trp	Lys	His	Glu	Lys	Cys	Asn				
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Ile	Thr	Met	Arg	Val	Trp	Leu	Gly	Leu	Ser	Gln	His	Ser	Val	Asp				
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Cys	Pro	Ser	Ser	Thr	Trp	Ile	Gln	Phe	Gln	Asp	Ser	Cys	Tyr	Ile				
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Phe	Leu	Gln	Glu	Ala	Ile	Lys	Val	Glu	Ser	Ile	Glu	Asp	Val	Arg				
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Lys	Trp	Thr	Asp	Gln	Asp	Asp	Asp	Glu	Asp	Leu	Val	Asp	Thr	Cys		
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Ala	Phe	Leu	His	Ile	Lys	Thr	Gly	Glu	Trp	Lys	Lys	Gly	Asn	Cys		
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Tyr	Lys	Arg	Lys	Tyr	Leu	Ser	Asp	Asn	His	Ile	Leu	Ile	Ser	Ala		
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Leu	Val	Ile	Ala	Ser	Thr	Val	Ile	Leu	Thr	Val	Leu	Gly	Ala	Ile		
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Ile	Trp	Phe	Leu	Tyr	Lys	Lys	His	Ser	Asp	Ser	Arg	Phe	Thr	Thr		
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Val	Phe	Ser	Thr	Ala	Pro	Gln	Ser	Pro	Tyr	Asn	Glu	Asp	Cys	Val		
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20                   25                   30

Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys  
35                   40                   45

Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp  
50                   55                   60

Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser

65

70

## SEQLIST\_DAVI257.002APC.TXT

75

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Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg  
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His  
100 105 110

His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly  
115 120 125

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly  
130 135 140

Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg  
145 150 155 160

Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp  
165 170 175

Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro  
180 185 190

Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile  
195 200 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu  
210 215 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp  
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Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser  
245 250 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile  
260 265 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly  
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Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro  
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Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met  
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Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp  
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Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn  
355 360 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys  
370 375 380

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His  
385 390 395 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp  
405 410 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr  
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Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp  
435 440 445

Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser  
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Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys  
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Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser  
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Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu  
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Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys  
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Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu  
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Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys  
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Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys  
610   615   620

Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp  
625   630   635   640

Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys  
645   650   655

Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu  
660   665   670

Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe  
675   680   685

Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln  
690   695   700

Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro  
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Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr  
725   730   735

Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys  
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Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe  
755   760   765

Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr  
770   775   780

Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr  
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Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu  
805   810   815

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Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala  
835 840 845

Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala  
850 855 860

Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp  
865 870 875 880

Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe  
885 890 895

Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp  
900 905 910

Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe  
915 920 925

Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp  
930 935 940

Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn  
945 950 955 960

Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala  
965 970 975

Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser  
980 985 990

Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala  
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Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn  
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Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro  
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Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu  
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Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys

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1060

1065

Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg  
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His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg  
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Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn  
 1100 1105 1110

Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys  
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Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp  
 1130 1135 1140

Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn  
 1145 1150 1155

Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn  
 1160 1165 1170

Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala  
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Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp  
 1190 1195 1200

Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala  
 1205 1210 1215

Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro  
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Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp  
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Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn  
 1250 1255 1260

Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln  
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Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys  
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Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu  
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Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala  
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Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser  
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Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu  
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Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu  
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Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe  
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Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val  
 1400 1405 1410

Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His  
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Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp  
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Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu Ser Ser  
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His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly Ser Thr  
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Phe Asp Tyr Ile Pro Trp Lys Gly Gln Thr Ser Pro Gly Asn Cys  
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Val Leu Leu Asp Pro Lys Gly Thr Trp Lys His Glu Lys Cys Asn  
 1490 1495 1500

Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Ser Lys  
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Lys Leu Ser Arg Leu Thr Tyr Ser Ser Arg Cys Pro Ala Ala Lys

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Ser Asp Gln Ala Leu His Ser Phe Ser Glu Ala Lys Lys Leu Cys  
1550                    1555                    1560

Ser Lys His Asp His Ser Ala Thr Ile Val Ser Ile Lys Asp Glu  
1565                    1570                    1575

Asp Glu Asn Lys Phe Val Ser Arg Leu Met Arg Glu Asn Asn Asn  
1580                    1585                    1590

Ile Thr Met Arg Val Trp Leu Gly Leu Ser Gln His Ser Val Asp  
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Cys Pro Ser Ser Thr Trp Ile Gln Phe Gln Asp Ser Cys Tyr Ile  
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Phe Leu Gln Glu Ala Ile Lys Val Glu Ser Ile Glu Asp Val Arg  
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Asn Gln Cys Thr Asp His Gly Ala Asp Met Ile Ser Ile His Asn  
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Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Lys Lys Gln Trp  
1655                    1660                    1665

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